

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 7, 2002, 15:40:21 : Search time 180.87 seconds
(without alignments)
499,786 Million cell updates/sec

Title: US-08-569-749-2

Sequence: 3277

1 MHRTASQRLPFGPSYONIKS.....LRKCFICRGIIKGVTFPLS 618

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP:archaea:*
2: SP:bacteria:*
3: SP:fungi:*
4: SP:human:*
5: SP:invertebrate:*
6: SP:mammal:*
7: SP:mnc:*
8: SP:organelle:*
9: SP:phase:*
10: SP:plant:*
11: SP:rodent:*
12: SP:virus:*
13: SP:vertebrate:*
14: SP:unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2630	80.3	589	11 Q9Q2C6	Q9Q2C6 ratius nov
2	2625	80.1	589	11 Q9Q2C6	Q9Q2C6 ratius nov
3	2339	71.4	610	13 Q57319	Q57319 gallus gall
4	2185	66.7	602	11 Q9Q2C6	Q9Q2C6 ratius nov
5	1678	51.2	1140	4 Q9Q2C6	Q9Q2C6 ratius nov
6	1138.5	34.7	324	13 Q9Q2C6	Q9Q2C6 ratius nov
7	898.5	27.4	501	11 Q9Q2C6	Q9Q2C6 ratius nov
8	898.5	27.4	501	11 Q9Q2C6	Q9Q2C6 ratius nov
9	898.5	27.4	501	11 Q9Q2C6	Q9Q2C6 ratius nov
10	898.5	27.4	501	11 Q9Q2C6	Q9Q2C6 ratius nov
11	801.5	24.3	195	13 Q9Q2C6	Q9Q2C6 ratius nov
12	796.5	24.3	195	13 Q9Q2C6	Q9Q2C6 ratius nov
13	494	15.1	597	11 Q9Q2C6	Q9Q2C6 ratius nov
14	490	15.0	438	5 Q9Q2C6	Q9Q2C6 ratius nov
15	486	14.8	281	12 Q9Q2C6	Q9Q2C6 ratius nov
16	481.5	14.7	379	5 Q9Q2C6	Q9Q2C6 ratius nov
17	476	14.5	264	12 Q9Q2C6	Q9Q2C6 ratius nov
18	475.5	14.5	276	12 Q9Q2C6	Q9Q2C6 ratius nov
19	470	14.3	261	12 Q9Q2C6	Q9Q2C6 ratius nov

20	466.5	14.2	377	5 Q9Q2C6	Q9Q2C6 ratius nov
21	462.5	14.1	280	4 Q9Q2C6	Q9Q2C6 ratius nov
22	460.5	14.1	298	4 Q9Q2C6	Q9Q2C6 ratius nov
23	423.5	12.9	313	12 Q9Q2C6	Q9Q2C6 ratius nov
24	368.5	11.2	268	12 Q9Q2C6	Q9Q2C6 ratius nov
25	363.5	11.1	268	12 Q9Q2C6	Q9Q2C6 ratius nov
26	287	8.8	80	4 Q9Q2C6	Q9Q2C6 ratius nov
27	240	7.3	292	12 Q9Q2C6	Q9Q2C6 ratius nov
28	239.5	7.3	210	4 Q9Q2C6	Q9Q2C6 ratius nov
29	231.5	7.1	284	12 Q9Q2C6	Q9Q2C6 ratius nov
30	222	6.8	305	12 Q9Q2C6	Q9Q2C6 ratius nov
31	220	6.7	301	12 Q9Q2C6	Q9Q2C6 ratius nov
32	194	5.9	4845	11 Q9Q2C6	Q9Q2C6 ratius nov
33	186.5	5.7	316	5 Q9Q2C6	Q9Q2C6 ratius nov
34	182	5.6	711	10 Q9Q2C6	Q9Q2C6 ratius nov
35	181.5	5.5	208	12 Q9Q2C6	Q9Q2C6 ratius nov
36	175.5	5.4	317	12 Q9Q2C6	Q9Q2C6 ratius nov
37	173.5	5.3	317	12 Q9Q2C6	Q9Q2C6 ratius nov
38	169	5.2	150	12 Q9Q2C6	Q9Q2C6 ratius nov
39	168.5	5.1	187	12 Q9Q2C6	Q9Q2C6 ratius nov
40	168	5.1	445	4 Q9Q2C6	Q9Q2C6 ratius nov
41	168	5.1	445	4 Q9Q2C6	Q9Q2C6 ratius nov
42	167	5.1	372	4 Q9Q2C6	Q9Q2C6 ratius nov
43	165	5.0	376	11 Q9Q2C6	Q9Q2C6 ratius nov
44	164	5.0	4804	5 Q9Q2C6	Q9Q2C6 ratius nov
45	161	4.9	155	12 Q9Q2C6	Q9Q2C6 ratius nov

ALIGNMENTS

RESULT 1	Q9Q2C6	PRELIMINARY	ERT: 569 AA.
ID	Q9Q2C6		
AC	Q9Q2C6		
DT	01-MAY-2000 (TREMBL)	13, Created	
DT	01-MAY-2000 (TREMBL)	13, Last sequence update	
DT	01-JUN-2001 (TREMBL)	17, Last annotation update	
DE	INITIATOR OF APOPTOSIS PROTEIN 2.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_Taxid=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=KIDNEY;		
RA	Dong Z., Denton M., Gu S.M., Salkumar P., Venkatachalam M.A.;		
RT	*Cloning of cDNA for rat inhibitor of apoptosis protein 2.*;		
RL	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.		
CC	-I- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.		
DR	EMBL	AF190020; AAF04585.1; -	
DR	HSPB	Q13490; 10B4.	
DR	Interpro	IPRO01370; BIR.	
DR	Interpro	IPRO01315; CARD.	
DR	Interpro	IPRO01841; Znf_fing.	
DR	Pfam	PF00653; BIR; 3.	
DR	Pfam	PF00619; CARD; 1.	
DR	Pfam	PF00097; zf-C3HC4; 1.	
DR	SMART	SM00238; BIR; 3.	
DR	SMART	SM00184; CARD; 1.	
DR	SMART	SM00184; CARD; 1.	
DR	PROSITE	PS01282; BIR_REPEAT_1; 3.	
DR	PROSITE	PS01043; BIR_REPEAT_2; 3.	
DR	PROSITE	PS02009; CARD; 1.	
KW	Zinc-finger.		
SO	SEQUENCE	589 AA; 66777 MW; E6012FEE3EA3142 CRC64;	

Query Match	80.3%; Score 2630; DB 11; Length 589;
Best Local Similarity	81.7%; Pred. No. 1.3e-177;
Matches	488; Conservative 53; Mismatches 48; Indels 8; Gaps 4;
QY	22 MEDSTLSDWNTSNKMKKVFSCSELYRMSYTFPAGVPSERSLARAGFYGVNDKY 81

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Db 1 MENSTVLASMTKREKMKITPDESCELTRKSTISAFPGVYSESLARAGFTYYGVNDKY 60
OY 82 KCFCGGLMDMKLGDSPTLOKHKQLYPSCSFIONIVASLGSTKNTSPMRNSFAHSLSP 141
Db 61 KCFCGGLMDMKKGDSPTPEKRRQFYPSCSFVOTLLSGGLQSAANKSPAKSRFAHSL-- 118
OY 142 TLEHSLPFGSSTSLSPNPLNSRAVEDISSRTNPYSTAMSTEARFLTYHMPLETLSP 201
Db 119 PLQO----GSHSLSPNPLNSRAVEDF--SLRMNPGSYAMSTEARFLTSYHMPLETLSP 173
OY 202 SELARAGFYTGPDYVACFACGCKLSNMPEKDDAMSEHRRHFPNCPFLNSETLTFRST 261
Db 174 AELAKAGFYTGGPDYVACFACGCKLSNMPEKDDPDLSEHRRHFPNCPFLNSETLTFRST 233
OY 262 SNLSQGTAAAMRTFMYPNPSSVPYOPOLASAGFYVGRNDVYKCFCCDGLRCMESGDD 321
Db 234 SNLSQGTAAAMRTFMYPNPSSVPYOPOLASAGFYVGRNDVYKCFCCDGLRCMESGDD 293
OY 322 PMVEHAKMFPPCEFLIRMKGOEFYDEIQGRYPHLLLEQLLSTSDTTGSENAADPPIIHFGPG 381
Db 294 PMIEHAKMFPPCEFLIRMKGOEFYDEIQGRYPHLLLEQLLSTSDTTGSENAADPPIIHFGPG 353
OY 382 ESSEDAVYMMNTPVYKSALEMGFNRLVQYVQSKITLTGTYVKTVDIVSALLANDEK 441
Db 354 E--NMEADVYMMNTPVYKSALEMGFNRLVQYVQSKITLTGTYVKTVDIVSALLANDEK 412
OY 442 REEKKRQAEKMSDLSLIRKNNMALFOQLCYPLIDDLLEASVLTKEBHDIRKQTO 501
Db 413 REEKKRQAEKMSDLSLIRKNNMALFOQLCYPLIDDLLEASVLTKEBHDIRKQTO 472
OY 502 IPLOARELIDITLVKGNMAANIFPNKCLKEIDSTLYKLVFNKMKMYIPEDVSGISLEEQ 561
Db 473 IPLOARELIDITLVKGNMAANIFPNKCLKEIDSTLYKLVFNKMKMYIPEDVSGISLEEQ 532
OY 562 LRLOEERTCYVCMDEKSVYVFTICGHLVYVOCBAPSLKRCPCIGITIKGTATFTLS 618
Db 533 LRLOEERTCYVCMDEKSVYVFTICGHLVYVOCBAPSLKRCPCIGITIKGTATFTLS 589

RESULT 2
OQESB8
ID 095B8 PRELIMINARY: PRT: 589 AA.
AC 095B8:
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE INHIBITOR OF APOPTOSIS PROTEIN 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RN 11
RA SEQUENCE FROM N.A.
RP Hoidal M., LeFebvre C.A., Hicks K., Korneluk R.G.;
RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of
RT Apoptosis protein 1, 2, and 3 Genes.*";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBD databases.
CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
Db EMBL: AF183431; AAC22971.1; -.
Db InterPro: IPR001370; BIR.
Db InterPro: IPR001841; znf_fing.
Db Pfam: PF00653; BIR. 3.
Db Pfam: PF00619; CARD. 1.
Db Pfam: PF00297; zf-C3HC4. 1.
Db SMART: SM00238; BIR. 3.
Db SMART: SM00114; CARD. 1.
Db SMART: SM00184; RING. 1.
Db PROSITE: PS01282; BIR_REPEAT_1; 1.
Db PROSITE: PS0143; BIR_REPEAT_2; 3.
Db PROSITE: PS0209; CARD. 1.
Db Zinc-finger.

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SQ SEQUENCE 589 AA: 66750 MW: 84F7089BD/CD285B CRC64:
Query Match 80.1%; Score 2625; DB 11; Length 589;
Best Local Similarity 81.6%; Pred. No. 2,9e-177;
Matches 487; Conservative 54; Mismatches 48; Indels 8; Gaps 4:

OY 22 MEDSTILSDWTNSNKKKKYDFSCELYRKSTYSPFPAGYVSESLARAGFTYYGVNDKY 81
Db 1 MENSTVLASMTKREKMKITPDESCELTRKSTISAFPGVYSESLARAGFTYYGVNDKY 60
OY 82 KCFCGGLMDMKLGDSPTLOKHKQLYPSCSFIONIVASLGSTKNTSPMRNSFAHSLSP 141
Db 61 KCFCGGLMDMKKGDSPTPEKRRQFYPSCSFVOTLLSGGLQSAANKSPAKSRFAHSL-- 118
OY 142 TLEHSLPFGSSTSLSPNPLNSRAVEDISSRTNPYSTAMSTEARFLTYHMPLETLSP 201
Db 119 PLQO----GSHSLSPNPLNSRAVEDF--SLRMNPGSYAMSTEARFLTSYHMPLETLSP 173
OY 202 SELARAGFYTGPDYVACFACGCKLSNMPEKDDAMSEHRRHFPNCPFLNSETLTFRST 261
Db 174 AELAKAGFYTGGPDYVACFACGCKLSNMPEKDDPDLSEHRRHFPNCPFLNSETLTFRST 233
OY 262 SNLSQGTAAAMRTFMYPNPSSVPYOPOLASAGFYVGRNDVYKCFCCDGLRCMESGDD 321
Db 234 SNLSQGTAAAMRTFMYPNPSSVPYOPOLASAGFYVGRNDVYKCFCCDGLRCMESGDD 293
OY 322 PMVEHAKMFPPCEFLIRMKGOEFYDEIQGRYPHLLLEQLLSTSDTTGSENAADPPIIHFGPG 381
Db 294 PMIEHAKMFPPCEFLIRMKGOEFYDEIQGRYPHLLLEQLLSTSDTTGSENAADPPIIHFGPG 353
OY 382 ESSEDAVYMMNTPVYKSALEMGFNRLVQYVQSKITLTGTYVKTVDIVSALLANDEK 441
Db 354 E--NMEADVYMMNTPVYKSALEMGFNRLVQYVQSKITLTGTYVKTVDIVSALLANDEK 412
OY 442 REEKKRQAEKMSDLSLIRKNNMALFOQLCYPLIDDLLEASVLTKEBHDIRKQTO 501
Db 413 REEKKRQAEKMSDLSLIRKNNMALFOQLCYPLIDDLLEASVLTKEBHDIRKQTO 472
OY 502 IPLOARELIDITLVKGNMAANIFPNKCLKEIDSTLYKLVFNKMKMYIPEDVSGISLEEQ 561
Db 473 IPLOARELIDITLVKGNMAANIFPNKCLKEIDSTLYKLVFNKMKMYIPEDVSGISLEEQ 532
OY 562 LRLOEERTCYVCMDEKSVYVFTICGHLVYVOCBAPSLKRCPCIGITIKGTATFTLS 618
Db 533 LRLOEERTCYVCMDEKSVYVFTICGHLVYVOCBAPSLKRCPCIGITIKGTATFTLS 589

RESULT 3
O57319
ID 057319 PRELIMINARY: PRT: 610 AA.
AC 057319:
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE INHIBITOR OF APOPTOSIS PROTEIN 1 (IAP) (INHIBITOR OF T CELL APOPTOSIS
DE PROTEIN).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
ON NCBI_TaxID=9031;
RN 11
RA SEQUENCE FROM N.A.
RP STRAIN-WHITE LECHORN; TISSUE-EMBRYONIC FIBROBLAST;
RC MEDLINE=98038801; PubMed=9372964;
RX You M., Ku P.-T., Hrdlickova R., Bose H.R. Jr.;
RT "ch-IAP, a member of the inhibitor-of-apoptosis protein family, is a
RT mediator of the antiapoptotic activity of the v-rel oncoprotein.*";
RL Mol. Cell Biol. 17:7328-7341(1997).
CC -1- FUNCTION: SUPPRESSOR OF APOPTOSIS IN ONCOPROTEIN V-REL-TRANSFORMED
CC CELLS.

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OY	369	ENAPRPIHFGCCSSSEDAVMMNTPVVASALENGFNRDLVYQGVQSILITGEGYKTV	428
Db	355	ETGEAAIVHGPGC-NMEDAVVMNTPVVAALADMGFSRSLSVHQVOROLITATGENRYTS	413
OY	429	DIVALLNAEDKEEKEERKKQAEMADSDLSIRKNMAYFOOLTCLVPLTLONLKANKY	488
Db	414	DLVLGLDMEDEMEEQTOGAEEESDDLTIRKRMVYLLOHLPTPTLDCILSKARYI	473
OY	489	NKOEHDIKOKTOPLOABELLDTLVKCNMAANTFPNCIKLEISDTLYKRLVENDNKYT	548
Db	474	TEOXYDAVAKRH-TLOATTLLDTVLAKNGTAATSPFNSTJOETIDPGRYDRIFVRONIRSI	532
OY	549	PTEEVSGLSLEBOLRIJOEBEPICVCAMDENVVFIPFCGLVWCOCAPSLKRCYCIRGI	608
Db	533	PTDDIAALPMEOBRKJOEBERTKCVCMDREASTLVTFPCGHVLCWCECAPSLKRCYCIGRT	592
OY	609	IKGTVRTPLS 618 	
Db	593	IKGTVRTPLS 602	
RESULT	5		
OJUNH1			
ID	OJUNH1	PRELIMINARY:	PRT: 1140 AA.
AC	OJUNH1		
DT	01-MAY-2000	(TREMBLrel. 13, Created)	
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)	
DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)	
De	API2-MLT FUSION PROTEIN.		
Gn	API2-MLT.		
Cn	API2-MLT.		
Os	Homo sapiens (Human).		
Oc	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Ox	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
Ox	NCBI_TaxId=9606;		
Rn	[1]		
Rp	SEQUENCE FROM N.A.		
Ra	DIERLINGE-99372400; PubMed-10339464;		
Ra	Liedlamm J., Baens M., Wlodarska I., Stefanova-Ouzounova M.,		
Ra	Hernandez J.M., Hossfeld D.K., De Wolf-Peeters C., Hagemeijer A.,		
Ra	Van den Berghe H., Marynen P.;		
Rt	"The apoptotic inhibitor gene API2 and a novel bcl gene, MLT, are		
Rt	frequently rearranged in the t(11;18)(q21;q21)psosociated with		
Rt	mucosa-associated lymphoid tissue lymphomas.";		
Rt	Blood 93;3601-3609(1999).		
Rt	-1 SIMILARITY: TO IMMUGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX		
Cc	DOMAIN.		
Cc	EMBL; AF123094; AAC64161.1; -.		
Cc	HSSP; Q13490; IOBH.		
Dr	InterPro: IPRO01370; BIR.		
Dr	InterPro: IPRO03576; Caspase.		
Dr	InterPro: IPRO01309; ICE_p20.		
Dr	InterPro: IPRO03598; IG_c2.		
Dr	InterPro: IPRO03600; IG_likc.		
Dr	InterPro: IPRO03006; IG_MHC.		
Dr	pfam; PF00653; BIR.3.		
Dr	pfam; PF00047; IG.2.		
Dr	SMART; SM00238; BIR.3.		
Dr	SMART; SM00115; CASc.1.		
Dr	SMART; SM00408; TCG2.1.		
Dr	SMART; SM00410; IG_likc.1.		
Dr	PROSITE; PS01282; BIR_REPEAT_1; 3.		
Dr	PROSITE; PS01413; BIR_REPEAT_2; 3.		
Dr	PROSITE; PS50208; CASPASE_P20; 1.		
OJ	SEQUENCE 1140 AA; 128758 MW; 0C18BD90287C723E CRC64;		

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Query Match:          51.2%; Score 1678; DB 4; Length 1140;  
Best Local Similarity 62.4%; Ped. No. 4, 8e-110;  
Matches 328; Conservative 61; Mismatches 105; Indels 32; Gaps 9.  
  
20 SIMEDTILSMQNTS-INOKKKDIFCELIYMYSTFPAQVPSERSIARCYITGN 78  
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
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D	b	2	NIENSIPLJNIMMSANFTELKJYDLSCELYRMSSTYSPFPAQVADVERSLARACGFYTVGN	61
Q	y	79	DKVACFCGMLMDMKJLQDSPKXHKOLYDSCSPFJONUYSA-SLGSRTKNTSP--NRMSF	1353
D	b	62	DKVACFCGMLMDMKKQDSPTEKHKKLYDSGRFQJSLNSVNNLATSQTPFPSSVTNS-	1200
Q	y	136	AHLSPTLEHSLSSGCSYSLSPNDLNSRAVEDISSGSHNPVSYAMSEPARATYUHWMP	1955
D	b	121	THSLPLGTENGSTYGRSYSNPSNPVNSRANOQPSALMSBSTYCMNNENARILLFPQWP	1800
Q	y	196	LTFPLSESLARAGYTYIGGDDVYACFPACGSKLSMNEKRDAMSEHRHPFNGCEPLSL-	254
D	b	181	LTFPLSTPLAKNGYTYIGGDDVYACFPACGSKLSMNEKRDAMSEHLRIFPKCFPIENQJ	2400
Q	y	255	ETLREISLISMOFHAAWRPNTWPSVPYVORLASAPFYXYGRNDYKCGCCDGLR	314
D	b	241	DTSRYSNLSHQHARKTTFNPPSSVLYANQDLSAQFTYVNSDPAKCCGCGGGR	3000
Q	y	315	CWMSGDDPVYEHAKWPFREELILMKQGEVDELOGKTRPILBOLLSTSTOTTEEMADP	374
D	b	301	CWMSGDDPVYQWAKWPFREYTRILRKQEEIKOVQYASPIHLBOLLSTSTODEMASS	360
Q	y	375	TIHFGGSSSEDAVMNTPVYKSALEMGFNLDVQOTVOSKILTGENTRYNDVSAL	4344
D	b	361	TIHFGGSEHSEDAIMNTPVYIAAEMGSSSLVQOTVYRKILTLTGENTRLVNDLYDL	420
Q	y	435	LNADEREEREKQAEWASDDLSILKRNRAAL-----FOOLTCLVPLIDMLKANVINK	490
D	b	421	LNADEREEREERATEEKESRKITVYNPPSKAVYLAQGFYKLC-----RATGHFP	471
Q	y	491	QEHDIKQKOTQIPQARELIDPLILYKQNAANAIFPNKJLAKIDSTLY	536
D	b	472	VOYQFMKAKKEIP-----NNNSSELF--NAVHNKADAGY	504

RESULT 6		PRELIMINARY:		PRT: 324 AA.	
OC	Q9DND2				
AC	Q9DND2				
DT	01-MAR-2001 (TRMBLrel. 16, Created)				
DT	01-MAR-2001 (TRMBLrel. 16, Last sequence update)				
DT	01-JUN-2001 (TRMBLrel. 17, Last annotation update)				
DE	APOPTOSIS INHIBITOR CH-1A1 (FRAGMENT).				
OS	Gallus gallus (chicken).				
OC	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;				
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;				
OC	Gallus.				
NCBI_TextID=9031;					
FN	11)				
RP	SEQUENCE FROM N.A.				
RA	Pendleton C.N., Bergmann W.J., Varadarajan J., Bose H.R. Jr.;				
RA	"The apoptosis inhibitor ch-1A1 is a direct transcriptional target of				
RL	v-rel and c-rel.";				
RL	Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF311289; AAG42316.1; .				
DR	Interfiro; IP8001370; BIR.				
DR	Pfam; PF00653; BIR; 3.				
DR	SMART; SM00238; BIR; 3.				
DR	PROSITE; PS01282; BIR_REPEAT_1; 1.				
DR	PROSITE; PS0143; BIR_REPEAT_2; 3.				
FT	NON_TER 324				
OC	SEQUENCE 324 AA; 36567 MW; 582B89DEAE3733F3 CRC64;				

	Query Match Count	31 / 78	Score	1138.5	DB	13	Length	324
	Best Local Similarity	63.4%	Pred. No.	1.2e-72				
	Matches	206	Conservative	49	Mismatches	55	Indels	15
					Gaps	6		
OY	20	SIMEDSTSLSDMNSKNO--KKMYDSEELRSTSYSTFEPPAPVPSERLARGPTTTCV	77					
		NINDESPPLASVMKQNAHCKEYLDTSCSELRYSTTSFTFPVPNVPYSERLRARAGCTTCG	61					
xy	78	NDEVCVFCCGGLMDNMKGSPLOKHROLYSFSSPFOUMLVSA-SLG-ST-----SKN	127					
db								

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Db 62 ODVKVCFSCGVLVDNMGPDGNAMEKHKOYDFVCSFVQMLSLNMLGSLTSHASPLVASN 121
Qy 128 TSPMRKSPALSHPTLHSHSLSPNPLNSRAVEDISSSTNPVSYAMSTEAR 187
Db 122 LSPSLRSM--TLSPFQVYFGSGFSFPDDVYTTAAEDLSHLRSLNPNMSTEAR 179
Qy 188 FLTYHMLPLTFPSBELARAGFYGGPCDRAFCGCKLSNNEKRDAMSEHRHPNC 247
Db 180 LRTFHMPLMELSPTELAKGLYYGTADKVCFCGGLSNMPEKRDAMSEHRHPNC 239
Qy 248 PLEENSL-ETLRFSISLSMOTHAARMETPMVPSVPVPEQLASAGFYVGRNDVRC 306
Db 240 PFENLMMDQGSFNVSNTVOTHEARVTEFLIMPRIPIVPEQLADAGFYVGRNDVRC 299
Qy 307 FCCDGLRCMSEGDPPWEHAKNFP 331
Db 300 FCCDGLRCMSEGDPPWEHAKNFP 324

RESULT 7
ID 086642 PRELIMINARY; PRT: 224 AA.
AC 086642;
DT 01-NOV-1998 (Tremblrel, 08, Created)
DT 01-NOV-1998 (Tremblrel, 08, last sequence update)
DT 01-JUN-2001 (Tremblrel, 17, last annotation update)
DE INHIBITOR OF APOPTOSIS PROTEIN (FRAGMENT).
GN KIAIP1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid:10116;
RN 11
RP SEQUENCE FROM N.A.
RA STRAIN-WISTAR; TISSUE-OVARY; CORPUS LUTEUM;
RA Bradley C.K., Lacher R.R., Dharmarajan A.M.;
RT Cloning and characterization of an inhibitor of apoptosis protein
RT (IAP) in the rat corpus luteum.
RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF304303; AAC32497.1;
DR HSPR; Q13450; J08H.
DR FICR; P00653; BIR_2.
DR SMART; SM00236; BIR; 2.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
FT NON_TER 224
PT SEQUENCE 224 AA; 25209 MW; 213A5234D5F856A CRC64;

Query Match: 28.9%; Score 945.5; DB 11; Length 224;
Best Local Similarity 74.9%; Pseq No.3,1e-59;
Matches 173; Conservative 18; Mismatches 33; Indels 7; Gaps 3;

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O9EQ05
ID O9EQ05 PRELIMINARY; PRT: 501 AA.
AC O9EQ05;
DT 01-MAR-2001 (Tremblrel, 16, Created)
DT 01-MAR-2001 (Tremblrel, 16, last sequence update)
DT 01-JUN-2001 (Tremblrel, 17, last annotation update)
DE INHIBITOR OF APOPTOSIS PROTEIN 3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid:10116;
RN 11
RP SEQUENCE FROM N.A.
RA STRAIN-WISTAR; TISSUE-OVARY;
RA Lacher R.R., Bradley C.K., Lacher M., Patis R.R., Dharmarajan A.M.;
RT Cloning, characterization and regulation of an inhibitor of apoptosis
RT protein in the rat corpus luteum.
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
DR EMBL; AF304333; AAC41192.1;
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00653; BIR; 3.
DR SMART; SM00236; BIR; 3.
DR SMART; SM00236; BIR; 3.
DR PROSITE; PS01282; BIR_REPEAT_1; 1.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
KW Zinc-finger.
SQ SEQUENCE 501 AA; 56548 MW; 0973FBF28B81C5A0 CRC64;

Query Match: 27.4%; Score 898.5; DB 11; Length 501;
Best Local Similarity 33.4%; Pred. No.1,8e-55;
Matches 204; Conservative 84; Mismatches 150; Indels 173; Gaps 15;

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QY		299	GRNDGKCFCCDGCEDSWPYNHAKVPRCEPLIPKCOEVEIDGKPIPLEO	358
Db		232	GEDDKKCFCHGGGLTDWKPSPBPZHAKVPGCGYLDEKQGEVINNI----	HLRHS 346
QY		359	IILSTDPVTEGNADNPRIIHFQPESSSDAVMNTFVVKSALEMGFNDDLVKOTVO&KIL	418
Db		347	LGSVYKRAEKT-----PSYTKLIDDTITFONMVQEAIRMGFNFRDKRTMEKLO	397
QY		419	TTCENKYTVNIVISALLAEDERKEBEKEQAE&NASDLSTLRKNMALEFOOLTCVLPI	478
Db		398	TTS&NSTLELYLTADVS&SN&DSODS-----	424
Dy		479	LDMALKANYINKE&HDIIKQTOIPLQARELDITLVKGNA&NIFRK&CLEIDS&TLRN	538
Dy		425	-----S&TOSILO-----	431
QY		539	LFDNRMKVPTEDBSV&SLPE&RLDREFFPKCYOMK&SV&VP&PC&HLYVC&B&CAPS	598
Db		432	-----KDST&E&DR&RLDRE&KLIC&MBRNALV&FV&PG&HLYVC&K&CA&VA	476
QY		599	L&RC&PIC&GI&IK&GV&TELPE	617
Db		477	VDR&C&PM&C&CTVITER&K&IT&RM	495
RESULT	11			
ID	QYIA69	PRELIMINARY:	PRT:	197 AA.
AC	QYIA69			
DT	01-OCT-2000	(TreeBLrel. 15, Created)		
DT	01-OCT-2000	(TreeBLrel. 15, Last sequence update)		
DT	01-JUN-2001	(TreeBLrel. 17, Last annotation update)		
DE		INITIATOR OF APOPTOSIS 1 (FRAGMENT).		
OC	BALBUS GALUS (CHICKEN).			
OC	Archaeopteryx, Meiodactylus, Chondrocladia, Gracilior, Vertepreter, Euletaoscomia,			
OC	Archaeopteryx, Aves, Neognathinae, Galliformes, Phasianidae, Psittacineae,			
OC	Gallus			
NCBI	TextID=9031:			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RC	STRAIN-BRED FAYOUPI: TISSUE=SPLEEN;			
RA	Zhou H., Lamont S.J.;			
RT	*Genetic variation among chicken lines and mammalian species in			
RT	*specific genes.*;			
RL	Submitted (Jan-2000) to the EMBL/GenBank/DDBJ databases.			
EMBL	AF221083: AAC35320.1;			
DR	InterPro: IPR001370; BIR.			
DR	pfam: PF00653; BIR; 2.			
DR	SMART: SM00238; BIR; 2.			
DR	PROSITE: PS01482; BIR-REPEAT_1; 2.			
DR	PROSITE: PS50143; BIR-REPEAT_2; 2.			
FT	NON_TER			
FT	1			
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QQ	SEQUENCE	197 AA: 22602 MW: D7932DAECF623E1A CRC64:		

[illegible]

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Db      182 EYLIRVKGGEFVSQV 197
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Q91A70
ID      Q91A70      PRELIMINARY;      PRT: 195 AA.
AC      Q91A70;
DC      01-OCT-2000 (TREMBLERel_15, Created)
DT      01-OCT-2000 (TREMBLERel_15, Last sequence update)
DT      01-JUN-2001 (TREMBLERel_17, Last annotation update)
DE      INHIBITOR OF APOPTOSIS 1 (FRAGMENT).
OS      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus
OX      NCBI_TaxID=9031;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-BREED LEGHORN; TISSUE=SPLEEN;
RA      Zhou H., Lamont S.J.;
RT      "Genetic variation among chicken lines and mammalian species in
RL      specific genes" in the EMBL/GenBank/DBJ databases.
RD      EMBL: AF221082; AAP35319.1; -.
DR      Litacitero, FR001370; BIR.
DR      Pirm; PR0053; BIR. 2.
DR      SMART; Sm00253; BIR. 2.
DR      PROSITE; PS01264; BIR_REPEAT_1. 2.
DR      PROSITE; PS50145; BIR_REPEAT_2. 2.
FT      NON_TER      1
FT      NON_TER      195
FT      NON_TER      195
SQ      SEQUENCE      195 AA; 22347 MW; 9C39EFA755E24E48 CRC64;

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	Query Match Similarity	24.3%	Score 796.5	DB 13	Length 195
	Best Local Similarity	68.2%	Pred. No. 8,6e-49		
	Matches 133	Conservative 33	Mismatches 28	Indels 1	Gaps 1
Oy	155	SLSLNPLNSRVEDISSSTNPYSVAMSTERARELTPLPLTFLSPSELARACFYTGP 214			
Db	1	SPDDVYVTTAAEDLSHRSKSLNPMSSTEARLRTPLFAMPLFLSPALAKKALYLTGT 60			
Oy	215	GDRVACFACGGKLSLNNEPKDASSEIRRHFFNCFLENSL-ETLRFSISNLSQTHAAM 273			
Db	61	ADKACFCTGGGSLNSNPPKDAENSRHRRHFFNCFLENSL-ETLRFSISNLSQTHAAM 120			
Oy	274	PTPEYAPSSVYVNPPEOLSAAFYVYGRNDYKCFCCGGISLNCSSDDPWEYHAKKFPFC 333			
Db	121	KFLNMPRIPIRVPPEQLADAGFYVYGRNDYKCFCCGGISLNCSSDDPWEYHAKKFPFC 180			
Oy	334	EFLIRKKGGEFVDEI 348			
Db	181	EYLLRVKGEFVSIV 195			
RESULT 13					
Q9R015					
ID	Q9R015	PREDIMINARY:	ERT:	597 AA.	
AC	Q9R015				
DT	01-MAY-2000	(7-EMBLrel. 13, Created)			
DR	01-MAY-2000	(7-EMBLrel. 17, Last sequence update)			
DEF	01-JUN-2001	(7-EMBLrel. 17, Last sequence update)			
GN	NEURONAL APOPTOSIS INHIBITORY PROTEIN.				
NC	BIRC6 OR NAIIP.				
OC	Mus musculus (Mouse).				
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	NCMammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
NCBI	TaxId=10090;				
FN	[1]				
RP	SEQUENCE FROM N.A.				
RA	MEDLINE=99431676; PubMed=10501978;				
FX	Huang S., Schart J.M., Gromey J.D., Enditzzi W.G., Dietrich W.F.,				


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QY 262 -----SNLSQTHA----- 270
Db 138 GANDSTLMEHNAVEGYIMSQLQSTGNNAVNAAGSYTGAAPQDPVYVNAHSTATQ 197
QY 271 -----AAKRTMFWSSVPVQPEOLASNGYVYGR 300
Db 198 ARGVDQPEICRPSAAGNYFPQYPAIETVARKTFEAMRYNLKQKPHQIALAGCFPTGV 257
QY 301 NDVYCCCKGKGLRCWESGDDPWVEHAKWPCFEELIRMGGEFVDEIQGRPHILBOLL 360
Db 258 GDRVRCSCGGGLMMDNDGEMBOHALMISQCFEVKIMKQGLVYIDTV----- 305
QY 361 STSDTGEENADPPIIHFGPGSSSDBAVMNMTPVVASALEMGFNRLVKQTVOSKILTT 420
Db 306 -----AAKPVLAEEKSESSIGV----- 324
QY 421 GENYTVNDIVSALLNAEDKREBEKROAEASDDLIRKNMALLFOQLTCVLPILD 480
Db 325 -----AVASTQASEEQOTSLSEEDVAGDA-----PSVAP--- 356
QY 481 NLKANYINKQEHDIKQKTOIPLQARLIDTILVKSNAAANIFNCKLEIDSTLYKNLE 540
Db 357 -----TAAFRIT-----NKI 366
QY 541 VKKNKKYIPTEDVSGLSLEBOLRLIOBERTCKVCKDEVSVPFPCGHLVWQECAPSRL 600
Db 367 VENTAVNPSTNSGST-----STPEKLCIKCYGAENVTAFLCGHVACAKCASSVT 420
QY 601 KCPICRGKGVYRTFLS 618
Db 421 KCPICRKPFQVRYEFS 438

RESULT 15
QYINL8
ID QYINL8 PRELIMINARY; PRT; 281 AA.
AC QYINL8;
DT 01-MAY-1999 (TEMBLrel, 10, Created)
DT 01-MAY-1999 (TEMBLrel, 10, Last sequence update)
DT 01-JUN-2001 (TEMBLrel, 17, Last annotation update)
DE IAP PROTEIN.
GN IAP.
OS Choristoneura fumiferana nuclear polyhedrosis virus (CFMPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=10448;
RN 111
RP SEQUENCE FROM N.A.
RC STRAIN=IRELAND;
KA Lauzon H., Aitl B.M., Ladd T., Palli R.;
RT "CFMPV IAP gene.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
DR EMBL; U62510; AAD0037.1; -.
DR HSSP; Q13490; 10BH.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; ZnF_ring.
DR Pfam; PF00653; BIR; 2.
DR Pfam; PF00097; zf-GHCD; 1.
DR SMART; SM00238; BIR; 2.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; UNKNOWN_1.
DR PROSITE; PS0143; BIR_REPEAT_2; 2.
KW Zinc_finger
SQ
SEQUENCE 281 AA: 32090 MW: 8209BE8A359F105E CRC64:

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Query Match 14.8%; Score 486; DB 12; Length 281;
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 Matches 112; Conservative 43; Mismatches 89; Indels 214; Gaps 6;
 181 MSTEBAFLTYHMHLPFLFSPSELARAGFYTGCDRVACFACGGKLSMWERKDDANSEH 240

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Db 14 MEDENARLATYTNWYVEFMSPROAMANGFYLLGKGDEYKCAFCKVEIRNMEASDDPARQH 73
QY 241 RRHFPNCPLIENSLIEFL-----RESISNL-----SQTIAAMRTFMV 278
Db 74 QKAPFOCPPLRRSGATLSAPOERAGLHAPOERATNQLSPPPAHKRYAIDAAALTFETE 133
QY 279 WPSVPVQPEOLASAGFYVYGRNDVYKPCDDGLRCWESGDDPWVEHAKWPCFEELIR 338
Db 134 WPRGLKORPEKLAAGFFYTGSRDVKCYCDGGLNDNBODDEMOOHALWFGCAVYLL 193
QY 339 MKGGEFVDEIQGRPHILEOLLSTSDTGEENADPPIIHFGPGSSSDBAVMNMTPVYS 398
Db 194 VKGRDYVQVY-----VTESCAIRDITV----- 214
QY 399 ALEMGFNRLVKQTVOSKILITGKNYKTVNDIVSALLNAEDKREBEKROAEASDDL 458
Db 215 -----KQGVYKHV----- 223
QY 459 SLIRKNMALLFOQLTCVLPILDNLKANYINKQEHDIKQKTOIPLQARLIDTILYGN 518
Db 224 -----YEP-----MLDPEKLCIKCYDE 241
QY 519 AAANIFKNCKLEIDSTLYKNLEVDKNMKYIPTEDVSGLSLEBOLRLIOBERTCKVCKDE 578
Db 224 -----YEP-----MLDPEKLCIKCYDE 241
QY 579 VSVVFTPCGHLVWQECAPSRLKCPICRGKGVYRTFLS 616
Db 242 KIVGFVPCGHLVWQECAPSRLKCPICRGKGVYRTFLS 279

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Search completed: January 7, 2002, 16:03:52
 Job time: 1411 sec

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